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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schlessinger, Joseph
Sap, Jan M.

(ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
PHOSPHATASE-ALPHA

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PENNIE & EDMONDS
(B) STREET: 1155 AVENUE OF THE AMERICAS
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/015,985
(B) FILING DATE: 10-FEB-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7683-020

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-9741/8864
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Ser	Trp	Phe	Ile	Leu	Val	Leu	Leu	Gly	Ser	Gly	Leu	Ile	Cys
1				5					10					15	
Val	Ser	Ala	Asn	Asn	Ala	Thr	Thr	Val	Ala	Pro	Ser	Val	Gly	Ile	Thr
		20						25					30		
Arg	Leu	Ile	Asn	Ser	Ser	Thr	Ala	Glu	Pro	Val	Lys	Glu	Glu	Ala	Lys
		35					40					45			
Thr	Ser	Asn	Pro	Thr	Ser	Ser	Leu	Thr	Ser	Leu	Ser	Val	Ala	Pro	Thr
		50				55					60				

Phe	Ser	Pro	Asn	Ile	Thr	Leu	Gly	Pro	Thr	Tyr	Leu	Thr	Thr	Val	Asn	65	70	75	80
Ser	Ser	Asp	Ser	Asp	Asn	Gly	Thr	Thr	Arg	Thr	Ala	Ser	Thr	Asn	Ser	85	90	95	
Ile	Gly	Ile	Thr	Ile	Ser	Pro	Asn	Gly	Thr	Trp	Leu	Pro	Asp	Asn	Gln	100	105	110	
Phe	Thr	Asp	Ala	Arg	Thr	Glu	Pro	Trp	Glu	Gly	Asn	Ser	Ser	Thr	Ala	115	120	125	
Ala	Thr	Thr	Pro	Glu	Thr	Phe	Pro	Pro	Ser	Gly	Asn	Ser	Asp	Ser	Lys	130	135	140	
Asp	Arg	Arg	Asp	Glu	Thr	Pro	Ile	Ile	Ala	Val	Met	Val	Ala	Leu	Ser	145	150	155	160
Ser	Leu	Leu	Val	Ile	Val	Phe	Ile	Ile	Ile	Val	Leu	Tyr	Met	Leu	Arg	165	170	175	
Phe	Lys	Lys	Tyr	Lys	Gln	Ala	Gly	Ser	His	Ser	Asn	Ser	Phe	Arg	Leu	180	185	190	
Ser	Asn	Gly	Arg	Thr	Glu	Asp	Val	Glu	Pro	Gln	Ser	Val	Pro	Leu	Leu	195	200	205	
Ala	Arg	Ser	Pro	Ser	Thr	Asn	Arg	Lys	Tyr	Pro	Pro	Leu	Pro	Val	Asp	210	215	220	
Lys	Leu	Glu	Glu	Glu	Ile	Asn	Arg	Arg	Met	Ala	Asp	Asp	Asn	Lys	Leu	225	230	235	240
Phe	Arg	Glu	Glu	Phe	Asn	Ala	Leu	Pro	Ala	Cys	Pro	Ile	Gln	Ala	Thr	245	250	255	
Cys	Glu	Ala	Ala	Ser	Lys	Glu	Glu	Asn	Lys	Glu	Lys	Asn	Arg	Tyr	Val	260	265	270	
Asn	Ile	Leu	Pro	Tyr	Asp	His	Ser	Arg	Val	His	Leu	Thr	Pro	Val	Glu	275	280	285	
Gly	Val	Pro	Asp	Ser	Asp	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Asn	Gly	Tyr	290	295	300	
Gln	Glu	Lys	Asn	Lys	Phe	Ile	Ala	Ala	Gln	Gly	Pro	Lys	Glu	Glu	Thr	305	310	315	320
Val	Asn	Asp	Phe	Trp	Arg	Met	Ile	Trp	Glu	Gln	Asn	Thr	Ala	Thr	Ile	325	330	335	
Val	Met	Val	Thr	Asn	Leu	Lys	Glu	Arg	Lys	Glu	Cys	Lys	Cys	Ala	Gln	340	345	350	
Tyr	Trp	Pro	Asp	Gln	Gly	Cys	Trp	Thr	Tyr	Gly	Asn	Ile	Arg	Val	Ser	355	360	365	
Val	Glu	Asp	Val	Thr	Val	Leu	Val	Asp	Tyr	Thr	Val	Arg	Lys	Phe	Cys	370	375	380	
Ile	Gln	Gln	Val	Gly	Asp	Met	Thr	Asn	Arg	Lys	Pro	Gln	Arg	Leu	Ile	385	390	395	400
Thr	Gln	Phe	His	Phe	Thr	Ser	Trp	Pro	Asp	Phe	Gly	Val	Pro	Phe	Thr	405	410	415	
Pro	Ile	Gly	Met	Leu	Lys	Phe	Leu	Lys	Lys	Val	Lys	Ala	Cys	Asn	Pro				

430

Gln	Tyr	Ala	Gly	Ala	Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg
		435					440					445			
Thr	Gly	Thr	Phe	Val	Val	Ile	Asp	Ala	Met	Leu	Asp	Met	Met	His	Thr
	450					455					460				
Glu	Arg	Lys	Val	Asp	Val	Tyr	Gly	Phe	Val	Ser	Arg	Ile	Arg	Ala	Gln
465					470					475					480
Arg	Cys	Gln	Met	Val	Gln	Thr	Asp	Met	Gln	Tyr	Val	Phe	Ile	Tyr	Gln
			485						490					495	
Ala	Leu	Leu	Glu	His	Tyr	Leu	Tyr	Gly	Asp	Thr	Glu	Leu	Glu	Val	Thr
			500					505					510		
Ser	Leu	Glu	Thr	His	Leu	Gln	Lys	Ile	Tyr	Asn	Lys	Ile	Pro	Gly	Thr
	515						520					525			
Ser	Asn	Asn	Gly	Leu	Glu	Glu	Glu	Phe	Lys	Lys	Leu	Thr	Ser	Ile	Lys
	530					535					540				
Ile	Gln	Asn	Asp	Lys	Met	Arg	Thr	Gly	Asn	Leu	Pro	Ala	Asn	Met	Lys
545					550					555					560
Lys	Asn	Arg	Val	Leu	Gln	Ile	Ile	Pro	Tyr	Glu	Phe	Asn	Arg	Val	Ile
			565						570					575	
Ile	Pro	Val	Lys	Arg	Gly	Glu	Glu	Asn	Thr	Asp	Tyr	Val	Asn	Ala	Ser
			580					585					590		
Phe	Ile	Asp	Gly	Tyr	Arg	Gln	Lys	Asp	Ser	Tyr	Ile	Ala	Ser	Gln	Gly
	595						600					605			
Pro	Leu	Leu	His	Thr	Ile	Glu	Asp	Phe	Trp	Arg	Met	Ile	Trp	Glu	Trp
	610					615					620				
Lys	Ser	Cys	Ser	Ile	Val	Met	Leu	Thr	Glu	Leu	Glu	Glu	Arg	Gly	Gln
625					630					635					640
Glu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Ser	Asp	Gly	Leu	Val	Ser	Tyr	Gly
				645					650					655	
Asp	Ile	Thr	Val	Glu	Leu	Lys	Lys	Glu	Glu	Glu	Cys	Glu	Ser	Tyr	Thr
			660					665					670		
Val	Arg	Asp	Leu	Leu	Val	Thr	Asn	Thr	Arg	Glu	Asn	Lys	Ser	Arg	Gln
		675					680					685			
Ile	Arg	Gln	Phe	His	Phe	His	Gly	Trp	Pro	Glu	Val	Gly	Ile	Pro	Ser
	690					695					700				
Asp	Gly	Lys	Gly	Met	Ile	Ser	Ile	Ile	Ala	Ala	Val	Gln	Lys	Gln	Gln
705					710					715					720
Gln	Gln	Ser	Gly	Asn	His	Pro	Ile	Thr	Val	His	Cys	Ser	Ala	Gly	Ala
				725					730					735	
Gly	Arg	Thr	Gly	Thr	Phe	Cys	Ala	Leu	Ser	Thr	Val	Leu	Glu	Arg	Val
			740					745					750		
Lys	Ala	Glu	Gly	Ile	Leu	Asp	Val	Phe	Gln	Thr	Val	Lys	Ser	Leu	Arg
		755					760					765			
Leu	Gln	Arg	Pro	His	Met	Val	Gln								

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATTCTTCT GGTTCATTCT TGTTCTGCTC GGCAGTGGTC TGATATGTGT CAGTGCCAAC	60
AATGCTACCA CAGTTGCACC TTCTGTAGGA ATTACAAGAT TAATTAAGTC ATCAACGGCA	120
GAACCAAGTTA AAGAAGAGGC CAAAAGTTCA AATCCAAGTT CTTCACTAAC TTCTCTTTCT	180
GTGGCACCAA CATTAGCCC AAATATAACT CTGGGACCCA CCTATTAAAC CACTGTCAAT	240
TCTTCAGACT CTGACAATGG GACCACAAGA ACAGCAAGCA CCAATTCTAT AGGCATTACA	300
ATTTACCAA ATGGAACGTG GCTTCAGAT AACCAGTTCA CGGATGCCAG AACAGAACCC	360
TGGGAGGGGA ATTCCAGCAC CGCAGCAACC ACTCCAGAAA CTTTCCCTCC TTCAGGTAAT	420
TCTGACTCGA AGGACAGAAG AGATGAGACA CCAATTATTG CGGTGATGGT GGCCCTGTCC	480
TCTCTGCTAG TGATCGTGTT TATTATCATA GTTTTGTACA TGTTAAGGTT TAAGAAATAC	540
AAGCAAGCTG GGAGCCATTC CAATCTTTC CGCTTATCCA ACGGCCGCAC TGAGGATGTG	600
GAGCCCCAGA GTGTGCCACT TCTGGCCAGA TCCCCAAGCA CCAACAGGAA ATACCCACCC	660
CTGCCCCGTG ACAAGCTGGA AGAGGAAATT AACCGGAGAA TGGCAGACGA CAATAAGCTC	720
TTAGGGGAGG AATTCAACGC TCTCCCTGCA TGTCTATCC AGGCCACCTG TGAGGCTGCT	780
TCCAAGGAGG AAAACAAGGA AAAAAATCGA TATGTAAACA TCTTGCCTTA TGACCACTCT	840
AGAGTCCACC TGACACCGGT TGAAGGGGTT CCAGATTCTG ATTACATCAA TGCTTCATTC	900
ATCAACGGTT ACCAAGAAAA GAACAAATTC ATTGCTGCAC AAGGACCAAA AGAAGAAACG	960
GTGAATGATT TCTGGCGGAT GATCTGGGAA CAAAACACAG CCACCATCGT CATGGTTACC	1020
AACCTGAAGG AGAGAAAGGA GTGCAAGTGC GCCCAGTACT GGCCAGACCA AGGCTGCTGG	1080
ACCTATGGGA ATATTCGGGT GTCTGTAGAG GATGTGACTG TCCTGGTGGA CTACACAGTA	1140
CGGAAGTTCT GCATCCAGCA GGTGGGCGAC ATGACCAACA GAAAGCCACA GCGCCTCATC	1200
ACTCAGTTCC ACTTTACCAG CTGGCCAGAC TTTGGGGTGC CTTTACCCC GATCGGCATG	1260
CTCAAGTTCC TCAAGAAGGT GAAGGCCTGT AACCCTCAGT ATGCAGGGGC CATCGTGGTC	1320
CACTGCAGTG CAGGTGTAGG GCGTACAGGT ACCTTTGTCG TCATTGATGC CATGCTGGAC	1380
ATGATGCATA CAGAACGGAA GGTGGACGTG TATGGCTTTG TGAGCCGGAT CCGGGCACAG	1440
CGCTGCCAGA TGGTGCAAAC CGATATGCAG TATGTCTTCA TATACCAAGC CCTTCTGGAG	1500

CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA 1560
 ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA 1620
 ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG 1680
 AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG 1740
 CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG 1800
 GACTCCTATA TCGCCAGOCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG 1860
 ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG 1920
 GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG 1980
 GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC 2040
 ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG 2100
 GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG 2160
 CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG 2220
 ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC 2280
 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG 2340
 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC 2400
 TTCAAGTAA 2409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His
 1 5 10 15
 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr
 20 25 30
 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys
 35 40 45
 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr
 50 55 60
 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn
 65 70 75 80
 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser
 85 90 95
 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln
 100 105 110
 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 115 120 125

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

	485								490						495					
Asp Thr Glu Leu Glu Val Thr Ser Leu Glu Thr His Leu Gln Lys Ile 500 505 510	Tyr Asn Lys Ile Pro Gly Thr Ser Asn Asn Gly Leu Glu Glu Glu Phe 515 520 525	Lys Lys Leu Thr Ser Ile Lys Ile Gln Asn Asp Lys Met Arg Thr Gly 530 535 540	Asn Leu Pro Ala Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro 545 550 555 560	Tyr Glu Phe Asn Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn 565 570 575	Thr Asp Tyr Val Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp 580 585 590	Ser Tyr Ile Ala Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe 595 600 605	Trp Arg Met Ile Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr 610 615 620	Glu Leu Glu Glu Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser 625 630 635 640	Asp Gly Leu Val Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu 645 650 655	Glu Glu Cys Glu Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr 660 665 670	Arg Glu Asn Lys Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp 675 680 685	Pro Glu Val Gly Ile Pro Ser Asp Gly Lys Gly Met Ile Asn Ile Ile 690 695 700	Ala Ala Val Gln Lys Gln Gln Gln Ser Gly Asn His Pro Ile Thr 705 710 715 720	Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu 725 730 735	Ser Thr Val Leu Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe 740 745 750	Gln Thr Val Lys Ser Leu Arg Leu Gln Arg Pro His Met Val Gln Thr 755 760 765	Leu Glu Gln Tyr Glu Phe Cys Tyr Lys Val Val Gln Glu Tyr Ile Asp 770 775 780	Ala Phe Ser Asp Tyr Ala Asn Phe Lys 785 790		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGC GAGTGAGGCG CTGACAGGGA CTCGCGGGGG CATCTTGCAC AGACCCCTGG	60
ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCCGCTTCTC CTCGCCATGG	120
AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT	180
GGGCCGAGAG CCCGGTCCTG AGGCGGAGCT GCCGTGCGCG TCCCCGCGG TCCCGCCCCA	240
GCGCCGGGCT CGGTCAGCAT GGATTCCTGG TTCATTCTTG TCCTGTTTGG CAGTGGTCTA	300
ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA	360
ATTAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAAA TTCAACCTCT	420
TCAGTAATTT CTCTTTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCACC	480
TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGC	540
GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCACG	600
GATGCCATAA CAGAACCCTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC	660
TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA	720
GTAATCGTGT TTATTATCAT AGTTCTGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT	780
GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCCAA	840
AGTGTAACAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG	900
GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA	960
GAATTCAACG CTCTCCCTGC TTGTCCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA	1020
GAAAACAAGG AAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC	1080
CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC	1140
TACCAGGAAA AGAACAATTT CATCGCTGCA CAAGGACCAA AAGAAGAAAC AGTGAATGAC	1200
TTCTGGAGAA TGATATGGGA ACAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG	1260
GAGAGAAAGG AGTGTAATG TGCCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG	1320
AATGTCCGTG TGTCTGTGCA GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC	1380
TCGATCCAGC AGGTGGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC	1440
CACTTCACCA GCTGGCCAGA CTTTGGGGTG CTTTTCACCC CAATTGGCAT GCTCAAGTTC	1500
CTCAAGAAGG TGAAGGCCTG TAACCCTCAG TACGCAGGGG CTATCGTGGT CCACTGCAGT	1560
GCAGGTGTAG GCGCACTGG CACCTTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT	1620
TCGGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCCA GCGCTGCCAG	1680
ATGGTACAGA CAGACATGCA GTACGTCTTC ATATACCAGG CCCTTCTGGA GCATTATCTG	1740
TATGGGGACA CAGAACTGGA AGTGACTTCT CTAGAAACCC ACCTACAAA AATTTATAAC	1800
AAGATCCCGG GGACTAGCAA CAACGGGTTA GAGGAGGAGT TTAAGAAATT AACTTCAATC	1860
AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG	1920

GTTTTACAGA TCATTCCATA TGAATTTAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA	1980
GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC	2040
ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCGAAT GATCTGGGAG	2100
TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT	2160
GCCCAGTACT GGCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG	2220
AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG	2280
AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC	2340
AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG	2400
GGGAACCATC CCATCACTGT GCACTGCAGT GCCGGGGCAG GACGGACAGG AACCTTCTGT	2460
GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT	2520
GTCAAGAGCC TCGGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATTC	2580
TGCTACAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA	2640
CAGGTGACAA GGCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTAATA TTCTGTTTTT	2700
GTTAATATAC CCAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC	2760
TATTACCTGT TAGATGGAGA TTTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTTCCA	2820
GTGTTTTATT GGGAAATTAA TAGTGTGATA TTTGGGTTGA TATAATGAAT TC	2872

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr	Asp	Tyr	Asn
1			5					10					15		
Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser	Asn	Tyr	Ile
		20						25					30		
Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	Lys	Tyr	Ile	Ala
		35					40					45			
Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp	Arg	Met	Ile
	50				55					60					
Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	Arg	Cys	Glu	Glu
65				70					75					80	
Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met	Glu	Glu	Gly
			85						90					95	
Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln	His	Lys	Arg
		100						105					110		
Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn	Lys	Lys	Glu

115	120	125
Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro		
130	135	140
Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu Arg Arg		
145	150	155
Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His		
165	170	175
Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala		
180	185	190
Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr		
195	200	205
Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala		
210	215	220
Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser	
1	5
Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile	
20	25
Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala	
35	40
Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile	
50	55
Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu	
65	70
Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp	
85	90
Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val	
100	105
Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr	
115	120
Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp	
130	135
Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu	
145	150
Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val	

165	170	175
His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp		
180	185	190
Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly		
195	200	205
Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp		
210	215	220
Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser	
1 5 10 15	
Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp	
20 25 30	
Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr	
35 40 45	
Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg	
50 55 60	
Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu	
65 70 75 80	
Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly	
85 90 95	
Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val	
100 105 110	
Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile	
115 120 125	
Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln	
130 135 140	
Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu	
145 150 155 160	
Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala	
165 170 175	
Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly	
180 185 190	
Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly	
195 200 205	
Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn	

210		215		220										
Tyr	Leu	Val	Gln	Thr	Glu	Gln	Tyr	Val	Phe	Ile	His	Asp	Thr	Leu
225				230				235						240
Val Glu														

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn	Lys	His	Lys	Asn	Arg	Tyr	Ile	Asn	Ile	Leu	Ala	Tyr	Asp	His	Ser
1				5					10					15	
Arg	Val	Lys	Leu	Arg	Pro	Leu	Pro	Gly	Lys	Asp	Ser	Lys	His	Ser	Asp
		20						25					30		
Tyr	Ile	Asn	Ala	Asn	Tyr	Val	Asp	Gly	Tyr	Asn	Lys	Ala	Lys	Ala	Tyr
		35					40					45			
Ile	Ala	Thr	Gln	Gly	Pro	Leu	Lys	Ser	Thr	Phe	Glu	Asp	Phe	Trp	Arg
	50					55					60				
Met	Ile	Trp	Glu	Gln	Asn	Thr	Gly	Ile	Ile	Val	Met	Ile	Thr	Asn	Leu
65					70					75					80
Val	Glu	Lys	Gly	Arg	Arg	Lys	Cys	Asp	Gln	Tyr	Trp	Pro	Thr	Glu	Asn
				85					90					95	
Ser	Glu	Glu	Tyr	Gly	Asn	Ile	Ile	Val	Thr	Leu	Lys	Ser	Thr	Lys	Ile
			100					105					110		
His	Ala	Cys	Tyr	Thr	Val	Arg	Arg	Phe	Ser	Ile	Arg	Asn	Thr	Lys	Val
		115					120					125			
Lys	Lys	Gly	Gln	Lys	Gly	Asn	Pro	Lys	Gly	Arg	Gln	Asn	Glu	Arg	Val
	130					135					140				
Val	Ile	Gln	Tyr	His	Tyr	Thr	Gln	Trp	Pro	Asp	Met	Gly	Val	Pro	Glu
145					150					155					160
Tyr	Ala	Leu	Pro	Val	Leu	Thr	Phe	Val	Arg	Arg	Ser	Ser	Ala	Ala	Arg
				165					170					175	
Met	Pro	Glu	Thr	Gly	Pro	Val	Leu	Val	His	Cys	Ser	Ala	Gly	Val	Gly
			180					185					190		
Arg	Thr	Gly	Thr	Tyr	Ile	Val	Ile	Asp	Ser	Met	Leu	Gln	Gln	Ile	Lys
		195					200					205			
Asp	Lys	Ser	Thr	Val	Asn	Val	Leu	Gly	Phe	Leu	Lys	His	Ile	Arg	Thr
	210					215					220				
Gln	Arg	Asn	Tyr	Leu	Val	Gln	Thr	Glu	Glu	Gln	Tyr	Ile	Phe	Ile	His
225					230					235					240
Asp Ala Leu Leu Glu															
245															

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser
 1           5           10          15
Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp
          20          25          30
Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr
          35          40          45
Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg
          50          55          60
Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu
65          70          75          80
Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly
          85          90          95
Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val
          100         105         110
Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr
          115         120         125
Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa
          130         135         140
Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly
          145         150         155         160
Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa
          165         170         175
Ala Ala Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala
          180         185         190
Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln
          195         200         205
Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His
          210         215         220
Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa
          225         230         235         240
Phe Ile His Xaa Ala Leu Xaa Glu
          245

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn	Val	Ile	Pro	Tyr	Asp	Tyr	Asn	1	5	10	15
Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu	Met	Ser	Lys	Glu	Ser	Glu	His	20	25	30	
Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp	Ser	Asp	Ser	Glu	Glu	Pro	Ser	35	40	45	
Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met	Ser	Tyr	Trp	Lys	Pro	Glu	Val	50	55	60	
Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys	Glu	Thr	Ile	Gly	Asp	Phe	Trp	65	70	75	80
Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys	Val	Ile	Val	Met	Leu	Thr	Glu	85	90	95	
Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys	Ala	Gln	Tyr	Trp	Gly	Glu	Gly	100	105	110	
Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val	Asp	Leu	Lys	Asp	Thr	Asp	Lys	115	120	125	
Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe	Glu	Leu	Arg	His	Ser	Lys	Arg	130	135	140	
Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr	Gln	Tyr	Thr	Asn	Trp	Ser	Val	145	150	155	160
Glu	Gln	Leu	Pro	Ala	Glu	Pro	Lys	Glu	Leu	Ile	Ser	Met	Ile	Gln	Val	165	170	175	
Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser	Ser	Glu	Gly	Asn	Lys	His	180	185	190	
His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys	Arg	Asp	Gly	Ser	Gln	Gln	195	200	205	
Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu	Leu	Glu	Ser	Ala	Glu	Thr	210	215	220	
Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val	Lys	Ala	Leu	Arg	Lys	Ala	225	230	235	240
Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln	Tyr	Gln	Phe	Leu	Tyr	Asp	245	250	255	
Val	Ile	Ala	Ser													260			

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn
1      5      10      15
Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val
20      25      30
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala
35      40      45
Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile
50      55      60
Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu
65      70      75      80
Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val
85      90      95
Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu
100     105     110
Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys
115     120     125
Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly
130     135     140
Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln
145     150     155     160
Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser
165     170     175
Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu
180     185     190
Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys
195     200     205
Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr
210     215     220
Glu Phe Cys Tyr Lys Val Val Gln Glu
225     230
  
```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:


```

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser
1      5      10      15
Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn
20      25      30
Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
35      40      45
Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp
50      55      60
Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met
65      70      75      80
Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn
85      90      95
Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu
100     105     110
Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr
115     120     125
Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp
130     135     140
Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val
145     150     155     160
Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp
165     170     175
Glu His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu
180     185     190
Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala
195     200     205
Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln
210     215     220
Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser
225     230

```

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala
1      5      10      15
Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile
20      25      30
Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Arg Ser Asn Glu Phe Ile Ile
35      40      45

```

Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile
50 55 60

Trp Asp His Asn Ala Gln Ile Ile Val Met Leu Pro Asp Asn Gln Ser
65 70 75 80

Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met
85 90 95

Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys
100 105 110

Leu Ser Asn Glu Glu Gln Ile Ile Ile His Asp Phe Ile Leu Glu Ala
115 120 125

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
130 135 140

Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn
145 150 155 160

Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His
165 170 175

Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr
180 185 190

Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val
195 200 205

Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu
210 215 220

Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: /label= Xaa
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn
1 5 10 15

Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Glu Gly Thr
35 40 45

Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu
50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp
 65 70 75 80
 Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa
 85 90 95
 Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Xaa Gln Tyr Trp Pro Ser Xaa
 100 105 110
 Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa
 115 120 125
 Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys
 130 135 140
 Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala
 145 150 155 160
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
 165 170 175
 Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser
 180 185 190
 Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala
 195 200 205
 Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa
 210 215 220
 Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu
 225 230 235 240
 Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met
 245 250 255
 Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Xaa Ile Glu Gln Tyr Gln
 260 265 270
 Phe Leu Tyr Lys Val Ile Leu Ser
 275 280